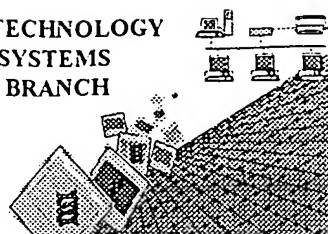BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/026,106A_

Source: _OIPE_

Date Processed by STIC: _7/23/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE USE THE CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/026,106A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
   Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
   Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
   "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
   (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
   (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
   (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:08

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\07232002\J026106A.raw

```
 1 <110> APPLICANT: Renauld, Jean-Christophe
 2        Fickensicher, Helmut
 3        Dumoutier, Laure
 4        Hor, Simon
 6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
 8 <130> FILE REFERENCE: LUD 5752 NDH
10 <140> CURRENT APPLICATION NUMBER: US/10/026,106A
12 <141> CURRENT FILING DATE: 2002-07-01
14 <160> NUMBER OF SEQ ID NOS: 19
```

Does Not Comply
Corrected Diskette Needed

see pp 1-7

ERRORED SEQUENCES

```
        32 <210> SEQ ID NO: 3
        33 <211> LENGTH: (20) 19 shown
        34 <212> TYPE: DNA
        35 <213> ORGANISM: Homo sapiens
W-->    36 <220> FEATURE:
W-->    37 <400> SEQUENCE: 3
E-->    38 aaggccatgg cgggcccga
        40 <210> SEQ ID NO: 4
        41 <211> LENGTH: (20) 19
        43 <212> TYPE: DNA
        44 <213> ORGANISM: Homo sapiens
W-->    45 <220> FEATURE:
W-->    46 <400> SEQUENCE: 4
E-->    47 cagaaggtca gtgctgaag
        65 <210> SEQ ID NO: 7
E-->    66 <211> LENGTH:
        67 <212> TYPE: DNA
        68 <213> ORGANISM: Homo sapiens
W-->    69 <220> FEATURE:
W-->    70 <400> SEQUENCE: 7
        71 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct      60
        72 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc     120
        73 gtgtacctga catggctcc cagggcttggc aacccccagg atgtgaccta ttttgtggcc     180
E-->    74 atcagagct ctcccacccg tagacggtgg cgcgaagtgg aagagtgtgc gggaaccaag       240
E-->    75 gagctgctat gttctatgat gtgcctgaag aaacaggacc tgtacaacaa gttcaaggga       300
E-->    76 cgcgtgcgga cggtttctcc cagctccaag tcccccctgg gtggagtccga atacctggat       360
E-->    77 tacctttttg aagtggagcc ggccccacct gtcctggtgc tcaccagac ggaggagat         420
E-->    78 cctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat       480
E-->    79 gaggtggcat tctggaagga gggggccgga aacaagaccc tatttccagt cactccccat        540
E-->    80 ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc        600
```

mandatory response needed (20) 19

(20) 19

(20) 19

(240) 239 number off

RAW SEQUENCE LISTING   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:08

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\07232002\J026106A.raw

```
E--> 81 agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc   660
E--> 82 ttgctggagg tcccagaagc caactgggct ttcctggtgc tgccatcgct tctgatactg   720
E--> 83 ctgttagtaa ttgccgcagg gggtgtgatc tggaagaccc tcatggggaa cccctggttt   780
E--> 85 cagcgggcaa agatgccacg ggccctggac ttttctggac acacacaccc tgtggcaacc   840
E--> 86 tttcagccca gcagaccaga gtccgtgaat gacttgttcc tctgtcccca aaaggaactg   900
E--> 87 accagagggg tcaggccgac gcctcgagtc agggccccag ccacccaaca gacaagatgg   960
E--> 88 aagaaggacc ttgcagagga cgaagaggag gaggatgagg aggacacaga agatggcgtc  1020
E--> 89 agcttccagc cctacattga accaccttct ttcctggggc aagagcacca ggctccaggg  1080
E--> 90 cactcggagg ctggtggggt ggactcaggg aggcccaggg ctcctctggt cccaagcgaa  1140
E--> 91 ggctcctctg cttgggattc ttcagacaga agctgggcca gcactgtgga ctcctcctgg  1200
E--> 92 gacagggctg ggtcctctgg ctatttggct gagaaggggc caggccaagg gccgggtggg  1260
E--> 93 gatgggcacc aagaatctct cccaccacct gaattctcca aggactcggg tttcctggaa  1320
E--> 94 gagctcccag aagataacct ctcctcctgg gccacctggg gcaccttacc accggagccg  1380
E--> 95 aatctggtcc ctgggggacc cccagtttct cttcagacac tgaccttctg ctgggaaagc  1440
E--> 96 agccctgagg aggaagagga ggcgagggaa tcagaaattg aggacagcga tgcgggcagc  1500
E--> 97 tggggggctg agagcaccca gaggaccgag gacaggggcc ggacattggg gcattacatg  1560
E--> 98 gccaggtgag ctgtcccccg acatcccacc gaatctgatg  1600
    101 <210> SEQ ID NO: 8
    102 <211> LENGTH: 522
    103 <212> TYPE: PRT
    104 <213> ORGANISM: Homo sapiens
W--> 105 <220> FEATURE:
W--> 106 <400> SEQUENCE: 8
    107 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 108
                             5                          10
    109 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 110
                20                          25                          30
    111 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 112              35                          40                          45
    113 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 114         50                          55                          60
    115 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 116
    65                      70                          75
    117     Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 118
                    85                          90
    119 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 120              100                         105                        110
    121 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 122         115                         120                        125
    123 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 124     130                         135                        140
    126 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 127 145                         150                        155     160
    128 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 129
                    165                         170                        175
    130 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
E--> 131         180                         185                        190
    132 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
```
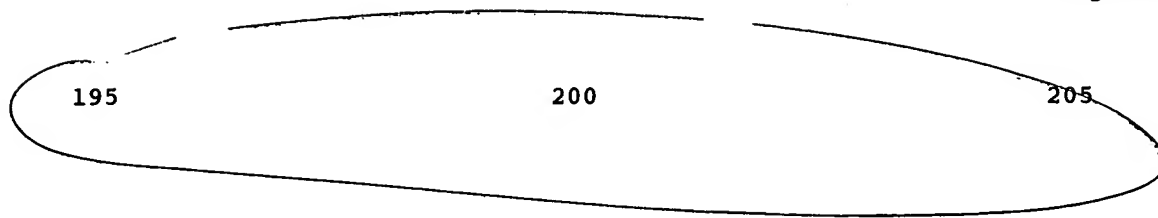
E-·-> 133   195   200   205

misaligned

220 nos.

```
    134 Ser Val Pro  Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 135         210                          215                       220
    136 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 137
225                         230                          235                         2
    138 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 139
                        245                          250                         255
    140 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 141
                        260                          265                         270
    142 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 143                 275                          280                         285
    144 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 145         290                          295                         300
    146 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 147
305                         310                          315
    148 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 149
                        325                          330                         33
    150 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 151                 340                          345                         350
    152 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 153                 355                          360                         365
    154 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 155         370                          375                         380
    156 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 157
385                         390                          395                         400
    158 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 159
                        405                          410                         415
    160 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 161                 420                          425                         430
    162 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 163                 435                          440                         445
    164 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
E--> 165         450                          455                         460
    168 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 169
465                         470                          475                         4
    170 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 171
                        485                          490                         495
    172 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 173
                        500                          505                         510
E--> 174
Gly Arg Thr Leu Gly His Tyr Met Ala Arg .       515                         520
    212 <210> SEQ ID NO: 10
    213 <211> LENGTH: 244
    214 <212> TYPE: PRT
```

```
    215 <213> ORGANISM: Homo sapiens
W--> 216 <220> FEATURE:
W--> 217 <400> SEQUENCE: 10
    219 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 220
  1                         5                         10                                    1
    221 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 222
                  20                         25                         30
```

misaligned numbers

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\07232002\J026106A.raw

misaligned number

```
        223 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 224          35                        40                              45
        225 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 226          50                        55                    60
        227 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 228
65                              70                        75
        229 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 230
                        85                              90
        231 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 232                100                       105                       110
        233 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 234          115                       120                      125
        235 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 236        130                       135                   140
        237 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 238
145                             150                       155
        239 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 240
                        165                       170                       175
        241 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
E--> 242                180                       185                      190
        243 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 244          195                       200                      205
        245 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 246        210                       215                       220
        249 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 250
225                             230                       235                    2
        251 Arg Val Arg Glu
        261 <210> SEQ ID NO: 12
        262 <211> LENGTH: 20 21
        263 <212> TYPE: DNA
        264 <213> ORGANISM: Homo sapiens
W--> 265 <220> FEATURE:
W--> 266 <400> SEQUENCE: 12
E--> 267 aagaaggtgg ttcaatgttag                         20 21
        295 <210> SEQ ID NO: 16
        296 <211> LENGTH: 24
        297 <212> TYPE: DNA
        298 <213> ORGANISM: Homo sapiens
W--> 299 <220> FEATURE:
E--> 300 <400> SEQUENCE: 24 16  <— change to
        301 gctccatggg acgatgccgc tgtg                   24
```

see next page for more error

```
<210> 19
<211> 20
<212> DNA
<220>
<400>    19
cactgcattc tagttgtggt                                        20
<213> Homo sapiens
```
move up

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\07232002\J026106A.raw

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:3
L:38 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:19 SEQ:3
L:45 M:283 W: Missing Blank Line separator, <220> field identifier
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:4
L:47 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:19 SEQ:4
L:53 M:283 W: Missing Blank Line separator, <220> field identifier
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:61 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:66 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:74 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:239 SEQ:7
M:254 Repeated in SeqNo=7
L:98 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:1599 SEQ:7
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:174 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:512 SEQ:8
L:180 M:283 W: Missing Blank Line separator, <220> field identifier
L:181 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:257 M:283 W: Missing Blank Line separator, <220> field identifier
L:258 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:283 W: Missing Blank Line separator, <220> field identifier
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:21 SEQ:12
L:267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:21 SEQ:12
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:283 W: Missing Blank Line separator, <220> field identifier
L:282 M:283 W: Missing Blank Line separator, <400> field identifier
L:292 M:283 W: Missing Blank Line separator, <400> field identifier
L:299 M:283 W: Missing Blank Line separator, <220> field identifier
L:300 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:24
```

VERIFICATION SUMMARY   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:09

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\07232002\J026106A.raw**

```
L:300 M:283 W: Missing Blank Line separator, <400> field identifier
L:307 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:283 W: Missing Blank Line separator, <220> field identifier
L:316 M:283 W: Missing Blank Line separator, <400> field identifier
L:322 M:283 W: Missing Blank Line separator, <220> field identifier
L:323 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:323 M:283 W: Missing Blank Line separator, <400> field identifier
```